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L5	L4 and (PCR or polymerase chain reaction or amplify$)	14	L5
L4	L3 and known and unknown	28	L4
L3	L2 and first and second	112	L3
L2	compar? near5 population	135	L2
L1	first near5 individual near5 seocnd near5 individual	0	L1

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Search Results - Record(s) 1 through 10 of 14 returned.

☐ 1. 6403309 . 19 Mar 99; 11 Jun 02. Methods for detection of nucleic acid polymorphisms using peptide-labeled oligonucleotides and antibody arrays. Iris; Francois J.-M., et al. 435/6; 435/18 435/287.2 435/288.3 435/7.1 536/23.1 536/24.33. C12Q001/68 C12M001/34 C07H021/04 C07H021/02.

☐ 2. 6346381 . 22 Dec 98; 12 Feb 02. Prostate cancer gene. Cohen; Daniel, et al. 435/6; 435/91.1 435/91.2 536/23.1 536/24.3. C12Q001/68 C12P019/34 C07M021/02.

☑ 3. 6271002 . 04 Oct 99; 07 Aug 01. RNA amplification method. Linsley; Peter S., et al. 435/91.1; 435/4 435/5 435/6 435/7.1 435/91.2 436/501 536/23.4 536/24.3. C12P019/34.

☐ 4. 6265546 . 23 Jun 99; 24 Jul 01. Prostate cancer gene. Cohen; Daniel, et al. 530/350; 424/174.1 435/7.1. C07K001/00 A61K039/395 A01N037/18 G01N035/53.

☐ 5. 6242579 . 21 Mar 00; 05 Jun 01. Antigen found on a small subset of human hematopoietic cells which binds to monoclonal antibody MG1. Lawman; Michael J. P., et al. 530/395; 435/343.2 435/372 530/388.75 530/827. C07K001/00.

☐ 6. 6235474 . 14 Jul 98; 22 May 01. Methods and kits for diagnosing and determination of the predisposition for diseases. Feinberg; Andrew P.. 435/6; 435/91.2 536/23.1 536/24.31 536/24.33. C12Q001/68 C12P019/34 C07H021/02 C07H021/04.

☐ 7. 6225047 . 19 Jun 98; 01 May 01. Use of retentate chromatography to generate difference maps. Hutchens; T. William, et al. 435/5; 210/656 422/59 422/70 435/174 435/177 435/182 435/288.6 435/7.2 435/7.21 435/7.22 435/7.32 436/161 436/514 436/518 436/541 436/824 530/412 530/413 530/415 530/417. G01N033/543.

☐ 8. 6207810 . 16 Nov 93; 27 Mar 01. TRT1 polynucleotides, host cells and assays. McClelland; Michael, et al. 536/23.1; 435/325 435/6 435/69.1 436/501 536/24.1 536/24.3 536/24.31 536/24.32 536/24.33. C07H021/00.

☐ 9. 6110661 . 02 Oct 97; 29 Aug 00. Bioluminescent reporter bacterium. Lajoie; Curtis A., et al. 435/4; 435/252.3 435/252.31 435/252.33 435/252.34 435/29 435/30 435/69.1 435/8. C12Q001/00 C12Q001/66 C12Q001/02.

☐ 10. 6025336 . 15 Feb 96; 15 Feb 00. Determining exposure to ionizing radiation agent with persistent biological markers. Goltry; Kristin L., et al. 514/44; 435/1.1 435/35 435/6 435/7.1 435/7.2 436/57 436/58 436/63 436/64. C12Q001/68 C12Q001/16 G01N023/00 A01N043/04.

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Search Results - Record(s) 11 through 14 of 14 returned.

☐ 11. 5968784 . 15 Jan 97; 19 Oct 99. Method for analyzing quantitative expression of genes. Spinella; Dominic G., et al. 435/91.1; 435/6 435/810 435/91.4 435/91.51. C12P019/34 C12N015/64.

☑ 12. 5922535 . 07 Nov 95; 13 Jul 99. Identifying sequence differences in nucleic acid populations. Huo; Li. 435/6; 536/23.1 536/24.3. C12Q001/68 C07H021/02 C07H021/04.

☐ 13. 5846735 . 18 Apr 96; 08 Dec 98. Hepatitis C virus Fc-binding function. Stapleton; Jack T., et al. 435/7.1; 435/5 435/7.72 435/7.9 435/7.92 435/7.93 435/960 530/387.1 530/387.3 530/388.3 530/389.1 530/389.4 530/391.1 530/391.3 530/866. G01N033/53 G01N033/576 C07K016/00 C07K014/735.

☐ 14. 5747650 . 10 May 96; 05 May 98. P53AS protein and antibody therefor. Kulesz-Martin; Molly F.. 530/387.7; 530/387.1 530/388.8 530/389.1 530/389.2. C07K016/22 C07K016/30 C07K016/32 C07K016/06.

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Term	Documents
PCR.DWPI,EPAB,JPAB,USPT.	30508
PCRS.DWPI,EPAB,JPAB,USPT.	847
POLYMERASE.DWPI,EPAB,JPAB,USPT.	33800
POLYMERASES.DWPI,EPAB,JPAB,USPT.	4663
CHAIN.DWPI,EPAB,JPAB,USPT.	659558
CHAINS.DWPI,EPAB,JPAB,USPT.	164710
REACTION.DWPI,EPAB,JPAB,USPT.	1207250
REACTIONS.DWPI,EPAB,JPAB,USPT.	264748
AMPLIFY$	0
AMPLIFY.DWPI,EPAB,JPAB,USPT.	145001
AMPLIFYABLE.DWPI,EPAB,JPAB,USPT.	15
(L4 AND (PCR OR POLYMERASE CHAIN REACTION OR AMPLIFY$)).USPT,JPAB,EPAB,DWPI.	14

There are more results than shown above. Click here to view the entire set.

Previous Page Next Page

09/891,332

```
=> s non-templat##(P)polymerase#
L1          229 NON-TEMPLAT##(P) POLYMERASE#

=> s l and reduce#
L2       232218 L AND REDUCE#

=> l1 and reduc?
L1 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l1 and reduc?
L3           31 L1 AND REDUC?

=> s l31 and (3 terminus or 3 end)
) IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l3 and (terminus or end#)
L4           15 L3 AND (TERMINUS OR END#)

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5             8 DUP REM L4 (7 DUPLICATES REMOVED)

=> d l5 1-8 bib ab kwic

L5   ANSWER 1 OF 8     MEDLINE                              DUPLICATE 1
AN   2000422353     MEDLINE
DN   20368644   PubMed ID: 10908340
TI   The GAA*TTC triplet repeat expanded in Friedreich's ataxia impedes
     transcription elongation by T7 RNA polymerase in a length and supercoil
     dependent manner.
AU   Grabczyk E; Usdin K
CS   Section on Genomic Structure and Function, Laboratory of Molecular and
     Cellular Biology, National Institute of Diabetes and Kidney Diseases,
     National Institutes of Health, Bethesda, MD 20892-0830, USA..
     grabczyk@helix.nih.gov
SO   NUCLEIC ACIDS RESEARCH, (2000 Jul 15) 28 (14) 2815-22.
     Journal code: 0411011. ISSN: 1362-4962.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200009
ED   Entered STN: 20000915
     Last Updated on STN: 20010521
     Entered Medline: 20000907
AB   Large expansions of the trinucleotide repeat GAA*TTC within the first
     intron of the X25 (frataxin) gene cause Friedreich's ataxia, the most
     common inherited ataxia. Expansion leads to reduced levels of
     frataxin mRNA in affected individuals. Here we show that GAA*TTC tracts,
     in the absence of any other frataxin gene sequences, can reduce
     the amount of GAA-containing transcript produced in a defined in vitro
     transcription system. This effect is due to an impediment to elongation
     that forms in the GAA*TTC tract during transcription, a phenomenon that is
     exacerbated by both superhelical stress and increased tract length. On
     supercoiled templates the major truncations of the GAA-containing
     transcripts occur in the distal (3') end of the GAA repeat. To
     account for these observations we present a model in which an RNA
     polymerase advancing within a long GAA*TTC tract initiates the
```

transient formation of an R*R*Y intramolecular DNA triplex. The **non-template** (GAA) strand folds back creating a loop in the template strand, and the **polymerase** is paused at the distal triplex-duplex junction.

AB . . . within the first intron of the X25 (frataxin) gene cause Friedreich's ataxia, the most common inherited ataxia. Expansion leads to **reduced** levels of frataxin mRNA in affected individuals. Here we show that GAA*TTC tracts, in the absence of any other frataxin gene sequences, can **reduce** the amount of GAA-containing transcript produced in a defined in vitro transcription system. This effect is due to an impediment. . . stress and increased tract length. On supercoiled templates the major truncations of the GAA-containing transcripts occur in the distal (3') **end** of the GAA repeat. To account for these observations we present a model in which an RNA **polymerase** advancing within a long GAA*TTC tract initiates the transient formation of an R*R*Y intramolecular DNA triplex. The **non-template** (GAA) strand folds back creating a loop in the template strand, and the **polymerase** is paused at the distal triplex-duplex junction.

L5 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1999:461513 BIOSIS
DN PREV199900461513
TI A simple and efficient method to **reduce** nontemplated nucleotide addition at the 3' **terminus** of RNAs transcribed by T7 RNA polymerase.
AU Kao, C. (1); Zheng, M.; Rudisser, S.
CS (1) Department of Biology, Indiana University, 1001 East 3rd St., Bloomington, IN, 47405-3700 USA
SO RNA (New York), (Sept., 1999) Vol. 5, No. 9, pp. 1268-1272. ISSN: 1355-8382.
DT Article
LA English
SL English
AB DNA templates modified with C2'-methoxyls at the last two nucleotides of the 5' termini dramatically **reduced non-templated** nucleotide addition by the T7 RNA **polymerase** from both single- and double-stranded DNA templates. This strategy was used to generate several different transcripts. Two of the transcripts were demonstrated by nuclear magnetic resonance spectroscopy to be unaffected in their sequence. Transcripts produced from the modified templates can be purified with greater ease and should be useful in a number of applications.
TI A simple and efficient method to **reduce** nontemplated nucleotide addition at the 3' **terminus** of RNAs transcribed by T7 RNA polymerase.
AB DNA templates modified with C2'-methoxyls at the last two nucleotides of the 5' termini dramatically **reduced non-templated** nucleotide addition by the T7 RNA **polymerase** from both single- and double-stranded DNA templates. This strategy was used to generate several different transcripts. Two of the transcripts. . .
IT Methods & Equipment
NMR spectroscopy: analytical method, spectroscopic techniques: CB
IT Miscellaneous Descriptors
nontemplated nucleotide addition: **reduction**

L5 ANSWER 3 OF 8 MEDLINE DUPLICATE 2
AN 1998221154 MEDLINE
DN 98221154 PubMed ID: 9553077
TI Template strand switching by T7 RNA polymerase.
AU Rong M; Durbin R K; McAllister W T
CS Department of Microbiology and Immunology, Morse Institute for Molecular Genetics, State University of New York, Health Science Center, Brooklyn, New York 11203-2098, USA.

NC GM38147 (NIGMS)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Apr 24) 273 (17) 10253-60.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199805
ED Entered STN: 19980609
Last Updated on STN: 19980609
Entered Medline: 19980522
AB T7 RNA **polymerase** (RNAP) is able to traverse a variety of discontinuities in the template (T) strand of duplex DNA, including nicks, gaps, and branched junctions in which the 3' **end** of the T strand is not complementary to the **non-template** (NT) strand. The products represent a faithful copy of the T strand, with no insertions or deletions. On double-stranded templates having protruding 3' **ends** the **polymerase** is able to insert the free 3' **end** of the NT strand and to utilize this as a new T strand ("turn around transcription"), resulting in the anomalous production of high molecular weight transcripts. The capacity of T7 RNAP to bypass interruptions in the T strand depends upon the stability of the elongation complex. Sequences that are expected to stabilize a local RNA:DNA hybrid (such as the presence of a C6 tract in the T strand) dramatically **reduce** dissociation of the RNAP while still allowing the enzyme to insert a new 3' **end**. Similar effects on RNAP release are observed when the enzyme reaches the **end** of a template (i.e. when synthesizing runoff products), resulting in markedly different yields of RNA product during multiple rounds of transcription.
AB T7 RNA **polymerase** (RNAP) is able to traverse a variety of discontinuities in the template (T) strand of duplex DNA, including nicks, gaps, and branched junctions in which the 3' **end** of the T strand is not complementary to the **non-template** (NT) strand. The products represent a faithful copy of the T strand, with no insertions or deletions. On double-stranded templates having protruding 3' **ends** the **polymerase** is able to insert the free 3' **end** of the NT strand and to utilize this as a new T strand ("turn around transcription"), resulting in the anomalous. . . expected to stabilize a local RNA:DNA hybrid (such as the presence of a C6 tract in the T strand) dramatically **reduce** dissociation of the RNAP while still allowing the enzyme to insert a new 3' **end**. Similar effects on RNAP release are observed when the enzyme reaches the **end** of a template (i.e. when synthesizing runoff products), resulting in markedly different yields of RNA product during multiple rounds of. . .

L5 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 1997:244443 CAPLUS
DN 126:312768
TI Site-directed mutagenesis using a PCR-based staggered re-annealing method without restriction enzymes
AU Ailenberg, Menachem; Silverman, Mel
CS Univ. Toronto, Toronto, ON, Can.
SO BioTechniques (1997), 22(4), 624, 626, 628, 630
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton
DT Journal
LA English
AB We have described a novel PCR-based approach for the introduction of cohesive termini into a given sequence without the use of restriction enzymes. This method can be used for addn. of one or more bases of cohesive termini into a sequence. Also, it can be used for creation of new restriction sites for ligation into a plasmid in the region flanking the amplified piece. We were able to clone a 515-bp RNase H cDNA into

NotI sites of a plasmid using the principles of the staggered re-annealing method described in this communication. This method could also be used in site-directed mutagenesis for single-site addn. or for addn. (as in this study) or deletion of any sequence into genes under conditions compatible with PCRs. The procedure described here has obvious advantages compared to blunt-**end** ligation and offers an alternative approach to the overlap extension method. In addn., it utilizes only one PCR while the overlap extension uses two reactions overall. Consequently, the potential of error insertion to the amplified product is **reduced**. Note that Pfu DNA **polymerase** is an essential requirement in our method because this enzyme does not create **non-template** 3' overhangs as do other heat-stable DNA **polymerases** like Taq **polymerase**. Finally, it is worth commenting on a potential exptl. limitation of the method. Since this technique is ultimately dependent on efficient melting of DNA strands, its usefulness may gradually decline when creation of cohesive termini in cDNA longer then 500 bp is required. However, future development of improved melting protocols could overcome this limitation and enable splicing of longer DNA segments.

AB We have described a novel PCR-based approach for the introduction of cohesive termini into a given sequence without the use of restriction enzymes. This method can be used for addn. of one or more bases of cohesive termini into a sequence. Also, it can be used for creation of new restriction sites for ligation into a plasmid in the region flanking the amplified piece. We were able to clone a 515-bp RNase H cDNA into NotI sites of a plasmid using the principles of the staggered re-annealing method described in this communication. This method could also be used in site-directed mutagenesis for single-site addn. or for addn. (as in this study) or deletion of any sequence into genes under conditions compatible with PCRs. The procedure described here has obvious advantages compared to blunt-**end** ligation and offers an alternative approach to the overlap extension method. In addn., it utilizes only one PCR while the overlap extension uses two reactions overall. Consequently, the potential of error insertion to the amplified product is **reduced**. Note that Pfu DNA **polymerase** is an essential requirement in our method because this enzyme does not create **non-template** 3' overhangs as do other heat-stable DNA **polymerases** like Taq **polymerase**. Finally, it is worth commenting on a potential exptl. limitation of the method. Since this technique is ultimately dependent on efficient melting of DNA strands, its usefulness may gradually decline when creation of cohesive termini in cDNA longer then 500 bp is required. However, future development of improved melting protocols could overcome this limitation and enable splicing of longer DNA segments.

L5 ANSWER 5 OF 8 MEDLINE DUPLICATE 3
AN 95393470 MEDLINE
DN 95393470 PubMed ID: 7664337
TI T7 RNA polymerase bypass of large gaps on the template strand reveals a critical role of the nontemplate strand in elongation.
AU Zhou W; Reines D; Doetsch P W
CS Department of Biochemistry, Emory University School of Medicine, Atlanta, Georgia 30322, USA.
NC CA55896 (NCI)
GM46311 (NIGMS)
SO CELL, (1995 Aug 25) 82 (4) 577-85.
Journal code: 0413066. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199510
ED Entered STN: 19951020
Last Updated on STN: 19980206
Entered Medline: 19951006
AB We show that T7 RNA **polymerase** can efficiently transcribe DNA

containing gaps from one to five bases in the template strand. Surprisingly, broken template strands missing up to 24 bases can still be transcribed, although at **reduced** efficiency. The resulting transcripts contain the full template sequence with the RNA deleted for the gapped region missing on the template strand. These findings indicate that the **end** of a downstream template strand can be brought into the **polymerase** and transcribed as if it were a part of an intact polynucleotide chain by utilizing the unpaired nontemplate strand. This, as well as transcription of an intact template strand, relies heavily upon the **non-template** strand, suggesting that a duplex DNA-binding site on the leading edge of RNA **polymerase** is required for RNA chain elongation on DNA templates. This work contributes substantially to the emerging picture that the nontemplate strand is an important element of the transcription elongation complex.

AB We show that T7 RNA **polymerase** can efficiently transcribe DNA containing gaps from one to five bases in the template strand. Surprisingly, broken template strands missing up to 24 bases can still be transcribed, although at **reduced** efficiency. The resulting transcripts contain the full template sequence with the RNA deleted for the gapped region missing on the template strand. These findings indicate that the **end** of a downstream template strand can be brought into the **polymerase** and transcribed as if it were a part of an intact polynucleotide chain by utilizing the unpaired nontemplate strand. This, as well as transcription of an intact template strand, relies heavily upon the **non-template** strand, suggesting that a duplex DNA-binding site on the leading edge of RNA **polymerase** is required for RNA chain elongation on DNA templates. This work contributes substantially to the emerging picture that the nontemplate. . .

L5 ANSWER 6 OF 8 MEDLINE DUPLICATE 4
AN 94148953 MEDLINE
DN 94148953 PubMed ID: 8106475
TI Termination of transcription by RNA polymerase III from wheat germ.
AU Wang X; Folk W R
CS Department of Biochemistry, University of Missouri, Columbia 65212.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1994 Feb 18) 269 (7) 4993-5004.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199403
ED Entered STN: 19940330
Last Updated on STN: 19970203
Entered Medline: 19940322

AB A novel system has been established to study transcription by RNA **polymerase** III. Purified wheat germ RNA **polymerase** III will initiate transcription on SV40 DNA templates amplified by **polymerase** chain reaction. Transcription initiates primarily at a thymidine 3 residues from a PvuII **terminus** at nucleotide 272 and terminates at a downstream A8:T8 sequence at nucleotides 21-28. Termination is enhanced if the RNA **polymerase** is caused to pause downstream of the A8:T8 sequence, but termination is unaffected by upstream sequences. Transcription of heteroduplex DNA templates with mismatches in the A8:T8 sequence indicates that termination is dependent upon the integrity of the A8 sequence in the template strand and is only slightly affected by changes in the T8 sequence of the **non-template** strand. However, templates containing 2'-deoxyuridine or 5'-bromo-2'-deoxyuridine in place of thymidine in the **non-template** strand **reduce** termination efficiency, as does incorporation of 5'-bromouracil into RNA. There is no obvious correlation between DNA bending and termination efficiency.

AB A novel system has been established to study transcription by RNA **polymerase** III. Purified wheat germ RNA **polymerase** III

will initiate transcription on SV40 DNA templates amplified by **polymerase** chain reaction. Transcription initiates primarily at a thymidine 3 residues from a PvuII **terminus** at nucleotide 272 and terminates at a downstream A8:T8 sequence at nucleotides 21-28. Termination is enhanced if the RNA **polymerase** is caused to pause downstream of the A8:T8 sequence, but termination is unaffected by upstream sequences. Transcription of heteroduplex DNA. . . the A8 sequence in the template strand and is only slightly affected by changes in the T8 sequence of the **non-template** strand. However, templates containing 2'-deoxyuridine or 5'-bromo-2'-deoxyuridine in place of thymidine in the **non-template** strand **reduce** termination efficiency, as does incorporation of 5'-bromouracil into RNA. There is no obvious correlation between DNA bending and termination efficiency.

L5 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 1995:191125 CAPLUS
DN 122:2676
TI A high-yield modification of mutation by overlap extension using three primers
AU Dilsiz, Nihat; Crabbe, M. James C.
CS School Animal Microbial Sciences, University Reading, Whiteknights/Reading, RG6 2AJ, UK
SO Anal. Biochem. (1994), 222(2), 510-11
CODEN: ANBCA2; ISSN: 0003-2697
DT Journal
LA English
AB The template-independent terminal transferase activity of Taq **polymerase reduces** the efficiency of mutation by overlap extension using 4 primers, due to addn. of a single **non-template**-directed adenine at each 3'-**end** of the duplex PCR fragments. A modification is described which uses 3 primers in 2 steps, thereby obviating the inefficiency and resulting in the correct (mutated) base sequence at the 3' **end** of the PCR product. When applied to the lens membrane protein MIP26, the modified procedure increased the efficiency of mutagenesis from 80% to 100%. In addn., the yield of mutant PCR product increased from 200 ng/100.mu.L reaction for the 4-primer method to 1 .mu.L/100 .mu.L reaction for the 3-primer method.
AB The template-independent terminal transferase activity of Taq **polymerase reduces** the efficiency of mutation by overlap extension using 4 primers, due to addn. of a single **non-template**-directed adenine at each 3'-**end** of the duplex PCR fragments. A modification is described which uses 3 primers in 2 steps, thereby obviating the inefficiency and resulting in the correct (mutated) base sequence at the 3' **end** of the PCR product. When applied to the lens membrane protein MIP26, the modified procedure increased the efficiency of mutagenesis from 80% to 100%. In addn., the yield of mutant PCR product increased from 200 ng/100.mu.L reaction for the 4-primer method to 1 .mu.L/100 .mu.L reaction for the 3-primer method.

L5 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 1993:248889 CAPLUS
DN 118:248889
TI Toscana virus genomic L segment: molecular cloning, coding strategy and amino acid sequence in comparison with other negative strand RNA viruses
AU Accardi, Luisa; Gro, Maria Cristina; Di Bonito, Paola; Giorgi, Colomba
CS Lab. Virol., Ist. Super. Sanita, Rome, 00161, Italy
SO Virus Res. (1993), 27(2), 119-31
CODEN: VIREDF; ISSN: 0168-1702
DT Journal
LA English
AB The complete nucleotide sequence of Toscana (TOS) virus (Bunyaviridae, Phlebovirus) L segment was detd. The L segment is 6404 nucleotides long, contg. a single open **reducing** frame (ORF) in the viral

complementary sense coding for a protein of 2095 amino acids that, as in the case of neg. strand RNA viruses, could be part of the RNA **polymerase** of TOS virus. This ORF is expressed by a mRNA as long as the genomic segment. Like the mRNAs expressed by the genomic segments of the other Bunyaviruses, the L mRNA has **non-templated** sequences at the 5' **end**. The comparison of TOS L protein sequence with the corresponding sequences of other neg. strand RNA viruses showed a very high homol. only with the Rift Valley Fever (RVF) virus. The residues conserved between the two proteins are mainly concd. in the central region and contain three DD motifs proposed by Argos (1988) to be functional domains of DNA and RNA **polymerases**. The complete sequence of the Toscana virus L genomic segment has been deposited in the EMBL library with the accession no. X68414.

AB The complete nucleotide sequence of Toscana (TOS) virus (Bunyaviridae, Phlebovirus) L segment was detd. The L segment is 6404 nucleotides long, contg. a single open **reducing** frame (ORF) in the viral complementary sense coding for a protein of 2095 amino acids that, as in the case of neg. strand RNA viruses, could be part of the RNA **polymerase** of TOS virus. This ORF is expressed by a mRNA as long as the genomic segment. Like the mRNAs expressed by the genomic segments of the other Bunyaviruses, the L mRNA has **non-templated** sequences at the 5' **end**. The comparison of TOS L protein sequence with the corresponding sequences of other neg. strand RNA viruses showed a very high homol. only with the Rift Valley Fever (RVF) virus. The residues conserved between the two proteins are mainly concd. in the central region and contain three DD motifs proposed by Argos (1988) to be functional domains of DNA and RNA **polymerases**. The complete sequence of the Toscana virus L genomic segment has been deposited in the EMBL library with the accession no. X68414.

=>